

(C) Starting on a separate page, a marked-up version entitled: "Version with markings to show changes made."

It is not believed that extensions of time or fees for net addition of claims are required beyond those that may otherwise be provided for in documents accompanying this paper. However, if additional extensions of time are necessary to prevent abandonment of this application, then such extensions of time are hereby petitioned under 37 C.F.R. § 1.136(a), and any fees required therefor (including fees for net addition of claims) are hereby authorized to be charged to our Deposit Account No. 19-0036.

Amendments

Please amend the application as follows:

In the Claims:

(a) Please cancel claims 26, 28-35, 52 and 89-99, without prejudice to or disclaimer of the subject matter contained therein. Applicants reserve the right to prosecute these claims in one or more continuing applications.

(b) Please amend claims 100-102 as follows:

Please substitute the following claim 100 for ~~currently pending claim 100~~:

100. (Once amended) A method for synthesizing a double stranded nucleic acid molecule comprising:

G1

- GI
60104
- (a) mixing one or more nucleic acid templates with a polypeptide having polymerase activity and one or more primers comprising at least a first recombination site or portions thereof;
 - (b) incubating said mixture under conditions sufficient to synthesize a first nucleic acid molecule which is complementary to all or a portion of said one or more templates and which comprises at least said first recombination site or portions thereof; and
 - (c) incubating said first nucleic acid molecule in the presence of one or more primers comprising at least a second recombination site or portions thereof under conditions sufficient to synthesize a second nucleic acid molecule complementary to all or a portion to said first nucleic acid molecule, thereby producing a double stranded nucleic acid molecule comprising at least said first and second recombination sites or portions thereof,

wherein at least one of said first and second recombination sites comprises one or more mutations that remove one or more stop codons from said recombination sites.

~~Please substitute the following claim 101 for currently pending claim 101:~~

101. (Once amended) A method for synthesizing a double stranded nucleic acid molecule comprising:

- (a) mixing one or more nucleic acid templates with a polypeptide having polymerase activity and one or more primers comprising at least a first recombination site or portions thereof;

- (b) incubating said mixture under conditions sufficient to synthesize a first nucleic acid molecule which is complementary to all or a portion of said one or more templates and which comprises at least said first recombination site or portions thereof; and
- (c) incubating said first nucleic acid molecule in the presence of one or more primers comprising at least a second recombination site or portions thereof under conditions sufficient to synthesize a second nucleic acid molecule complementary to all or a portion to said first nucleic acid molecule, thereby producing a double stranded nucleic acid molecule comprising at least said first and second recombination sites or portions thereof,

wherein at least one of said first and second recombination sites comprises one or more mutations that avoids hairpin formation in said recombination sites.

~~Please substitute the following claim 102 for currently pending claim 102:~~

102. (Once amended) A method for synthesizing a double stranded nucleic acid molecule comprising:

- (a) mixing one or more nucleic acid templates with a polypeptide having polymerase activity and one or more primers comprising at least a first recombination site or portions thereof;
- (b) incubating said mixture under conditions sufficient to synthesize a first nucleic acid molecule which is complementary to all or a portion of said one or more templates and which comprises at least said first recombination site or portions thereof; and

- G1
cont.
- (c) incubating said first nucleic acid molecule in the presence of one or more primers comprising at least a second recombination site or portions thereof under conditions sufficient to synthesize a second nucleic acid molecule complementary to all or a portion to said first nucleic acid molecule, thereby producing a double stranded nucleic acid molecule comprising at least said first and second recombination sites or portions thereof,

wherein at least one of said first and second recombination sites comprises at least one nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-16 or a DNA sequence complementary thereto.

(c) Please enter the following new claims 118-127:

118. (New) A method for synthesizing a double stranded nucleic acid molecule comprising:

- G2
- (a) mixing one or more nucleic acid templates with a polypeptide having polymerase activity and one or more primers comprising at least a first recombination site or portions thereof;
- (b) incubating said mixture under conditions sufficient to synthesize a first nucleic acid molecule which is complementary to all or a portion of said one or more templates and which comprises at least said first recombination site or portions thereof; and
- (c) incubating said first nucleic acid molecule in the presence of one or more primers comprising at least a second recombination site or portions thereof under conditions sufficient to synthesize a second nucleic acid molecule complementary

to all or a portion to said first nucleic acid molecule, thereby producing a double stranded nucleic acid molecule comprising at least said first and second recombination sites or portions thereof,

wherein at least one of said first and second recombination sites comprises at least one nucleotide sequence that has at least 80-99% homology to a nucleotide sequence selected from the group of sequences consisting of SEQ ID NOs: 39-43, and a corresponding or complementary DNA or RNA sequence.

119. (New) A method for synthesizing a double stranded nucleic acid molecule comprising:

- G2
cont.
- (a) mixing one or more nucleic acid templates with a polypeptide having polymerase activity and one or more primers comprising at least a first recombination site or portions thereof;
 - (b) incubating said mixture under conditions sufficient to synthesize a first nucleic acid molecule which is complementary to all or a portion of said one or more templates and which comprises at least said first recombination site or portions thereof; and
 - (c) incubating said first nucleic acid molecule in the presence of one or more primers comprising at least a second recombination site or portions thereof under conditions sufficient to synthesize a second nucleic acid molecule complementary to all or a portion to said first nucleic acid molecule, thereby producing a double stranded nucleic acid molecule comprising at least said first and second recombination sites or portions thereof,

wherein at least one of said first and second recombination sites comprises at least one nucleotide sequence that has at least 80-99% homology to a nucleotide sequence selected from the group

of sequences consisting of SEQ ID NOs: 1-16, and a corresponding or complementary DNA or RNA sequence.

120. (New) The method of claim 118, wherein said recombination sites or portions thereof are located at or near one terminus of said double stranded nucleic acid molecule.

121. (New) The method of claim 119, wherein said recombination sites or portions thereof are located at or near one terminus of said double stranded nucleic acid molecule.

122. (New) The method of claim 118, further comprising amplifying said first and second nucleic acid molecules.

123. (New) The method of claim 119, further comprising amplifying said first and second nucleic acid molecules.

124. (New) The method of claim 118, wherein said recombination sites or portions thereof are located at or near one or both termini of said double stranded nucleic acid molecule.

125. (New) The method of claim 119, wherein said recombination sites or portions thereof are located at or near one or both termini of said double stranded nucleic acid molecule.

126. (New) The method of claim 118, wherein said first and second recombination sites do not recombine with each other.

G²
CDD⁺

127. (New) The method of claim 119, wherein said first and second recombination sites
do not recombine with each other.

G2
G104.